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Input file 17867consj Output File 17867tra
 Sequence length 3366

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      10      20      30      40      50      60      70
CCCCGCGTCCGGCATGATTAAAGATTAAATTCATGTATTGAAAAATTTGTTACAGACCCCATGTGACATAACTGGAGCCA
80      90     100     110     120     130     140     M   F   H
GTGCAGTGCATGAAGAAGACTACGAGATTAGCCTGGATATTAACTTGTCTTCTAGAGAATAGATTTC   146   3154
      146
TCT TCT GCA ATG GTT AAT TCA CAC AGA AAA CCA ATG TTT AAC ATT CAC AGA GGA TTT TAC   23
TGC TTA ACA GCC ATC TTG CCC CAA ATA TGC ATT TGT TCT CAG TTC TCA GTG CCA TCT AGT   43
TAT CAC TTC ACT GAG GAT CCT GGG GCT TFC CCA GTA GCC ACT AAT GGG GAA CGA TTT CCT   63
TGG CAG GAG CTA AGG CTC CCC AGT GTG GTC ATT CCT CTC CAT TAT GAC CTC TTT GTC CAC   83
CCC AAT CTC ACC TCT CTG GAC TTT GTT GCA TCT GAG AAG ATC GAA GTC TTG GTC AGC AAT   103
GCT ACC CAG TTT ATC ATC TTG CAC AGC AAA GAT CTT GAA ATC ACG AAT GCC ACC CTT CAG   123
TCA GAG GAA GAT TCA AGA TAC ATG AAA CCA GGA AAA GAA CTG AAA GTT TTG AGT YAC CCT   143
GCT CAT GAA CAA ATT GCA CTG CTG GTT CCA GAG AAA CTT ACG CCT CAC CTG AAA TAC TAT   163
GTG GCT ATG GAC TTC CAA GCC AAG TTA GGT GAT GGC TTT GAA GGG TTT TAT AAA AGC ACA   183
TAC AGA ACT CTT GGT GGT GAA ACA AGA ATT CTT GCA GTA ACA GAT TTT GAG CCA ACC CAG   203
GCA CGC ATG GCT TTC CCT TGC TTT GAT GAA CCG TTG TTC AAA GCC AAC TTT TCA ATC KAG   223
ATA CGA AGA GAG AGC AGG CAT ATT GCA CTA TCC AAC ATG CCA AAG GTT AAG ACA ATT GAA   243
CTT GAA GGA GGT CTT TTG GAA GAT CAC TTT GAA ACT ACT GTA AAA ATG AGT ACA TAC CTT   263
GTA GCC TAC ATA GTT TGT GAT TTC CAC TCT CTG AGT GGC TTC ACT TCA TCA GGG GTC KAG   283
GTG TCC ATC TAT GCA TCC CCA GAC AAA CGG AAT CAA ACA CAT TAT GCT TTG CAG GCA TCA   303
CTG AAG CTA CTT GAT TTT TAT GAA KAG TAC TTT GAT ATC TAC TAT CCA CTC TCC AAA CTG   323
GAT TTA ATT GCT ATT CCT GAC TTT GCA CCT GGA GCC ATG GAA AAT TGG GGC CTC ATT TCA   343
TAT AGG GAG ACG TCA CTG CTT TTT GAC CCC AAG ACC TCT TCT GCT TCC GAT AAA CTG TGG   363
GTC ACC AGA GTC ATA GCC CAT GAA CTG GCG CAC CAG TGG TTT GCG AAC CTG GTC ACA ATG   383

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FIG. 1A.

10039073.123101

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GAA TGG TGG AAT GAT ATT TGG CTT AAG GAG GGT TTT GCA AAA TAC ATG GAA CTT ATC GCT 1203
 GTT AAT GCT ACA TAT CCA GAG CTG CAA TTT GAT GAC TAT TTT TTG AAT GTG TGT TTT GAA 1263
 GTA ATT ACA AAA GAT TCA TTG AAT TCA TCC CGC CCT ATC TCC AAA CCA GCG GAA ACC CCG 1323
 ACT CAA ATA CAG GAA ATG TTT GAT GAA GTT TCC TAT AAC AAG GGA GCT TGT ATT TTG AAT 1383
 ATG CTC AAG GAT TTT CTG GGT GAG GAG AAA TTC CAG AAA GGA ATA ATT CAG TAC TTA AAG 1443
 AAG TTC AGC TAT AGA AAT GCT AAG AAT GAT GAC TTG TGG AGC AGT CTG TCA AAT AGT TGT 1503
 TTA GAA AGT GAT TTT ACA TCT GGT GGA GTT TGT CAT TCG GAT CCC AAG ATG ACA AGT AAC 1563
 ATG CTC ACC TTT CTG GGG GAA AAT GCA GAG GTC AAA GAG ATG ATG ACT ACA TGG ACT CTC 1623
 CAG AAA GGA ATC CCC CTG CTG GTG GTT AAA CAA GAC GGG TGT TCA CTC CGA CTG CAA CAG 1683
 GAG CGC TTC CTC CAG GGG GTT TTC CAG GAA GAC CCT GAA TGG AGG GCC CTG CAG GAG AGG 1743
 TAC CTG TGG CAT ATC CCA TTG ACC TAC TCC ACG AGT TCT TCT AAT GTG ATC HAC AGA HAC 1803
 ATT CTA AAA TCA AAG ACA GAT ACT CTG GAT CTA CCT GAA AAG ACC AGT TGG GTG AAA TTT 1863
 AAT GTG GAC TCA AAT GGT TAC TAC ATC GTT CAC TAT GAG GGT CAT GGA TGG GAC CAA CTC 1923
 ATT ACA CAG CTG AAT CAG AAC CAC ACA CTT CTC AGA CCT AAG GAC AGA GTA GGT CTG ATT 1983
 CAT GAT GTG TTT CAG CTA GTT GGT GCA GGG AGA CTG ACC CTA GAC AAA GCT CTT GAC ATG 2043
 ACT TAC TAC CTC CAA CAT GAA ACA AGC AGC CCC GCA CTT CTC GAA GGT CTG AGT TAC TTG 2103
 GAA TCG TTT TAC CAC ATG ATG GAC AGA AGG AAT ATT TCA GAT ATC TCT GAA AAC CTC AAG 2163
 CGT TAC CTT CTT CAG TAT TTT AAG CCA GTG ATT GAC AGG CAA AGC TGG AGT GAC AAG GGC 2223
 TCA GTC TGG GAC AGG ATG CTC CGC TCG GCT CTC TTG AAG CTG GCC TGT GAT CTG AAC CAT 2283
 GCT CCT TGC ATC CAG AAA GCT GCT GAA CTC TTC TCC CAG TGG ATG GAA TCC AGT GGA AAA 2343
 TTA AAT ATA CCA ACA GAT GTT TTA AAG ATT GTG TAT TCT GTG GGT GCT CAG ACA ACA GCA 2403
 GGA TGG AAT TAC CTT TTA GAG CAA TAT GAA CTG TCA ATG TCA AGT GCT GAA CAA AAC AAA 2463

FIG. 1B.

10026073-123101

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ATT CTG TAT GCT TTG TCA ACG AGC AAG CAT CAG GAA AAG TTA CTG AAG TTA ATT GAA CTA 2529
 GGA ATG GAA GGA AAG GTT ATC AAG ACA CAG AAC TTG GCA GCT CTC CTT CAT GCG ATT GCC 2589
 AGA CGT CCA AAG GGG CAG CAA CTA GCA TGG GAT TTT GTA AGA GAA AAT TGG ACC CAT CTT 2649
 CTG AAA KAA FTT D GAC TTG GGC TCA TAT D GAC ATA AGG ATG ATC ATC TCT GGC ACA ACA A GCT 2709
 H CAC TTT TCT TCC AAG GAT AAG TTG CAA GAG GTG AAA CTA TTT TTT GAA TCT CTT GAG GCT 2769
 CAA GGA TCA CAT CTG GAT ATT TTT CAA ACT GTT CTG GAA ACG ATA ACC AAA AAT ATA AAA 2829
 V TGG CTG GAG AAG AAT CTT CCG ACT CTG AGG ACT TGG CTA ATG GTT AAT ACT TAA 2883
 ATGGTCAATAGAAAAAGTAGGCTGGGCGGGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCTGAGAAGGGCGGA
 TCACGAGGTCAGGAGATGGAGACCATCTGGCTAACACGGTGAGACCCGCTCCGCTAAAAATACAAAAAATTAGCCG
 GGCATGGTGGCAGGTGCCTGTAGTCCAGCTACTCGGCAGGCTGCAGCAGGAAAAATGGCATAAACCCGGGAGGTGGAGC
 TTGCAGTGAGCCGAGATTGCACCACTGCATTCCAGCCTGGGTGACTGAGCGAGACTCTGTCTCAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIG. 1C.

10039073.123104

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Analysis of sequence7420 (960 aa)

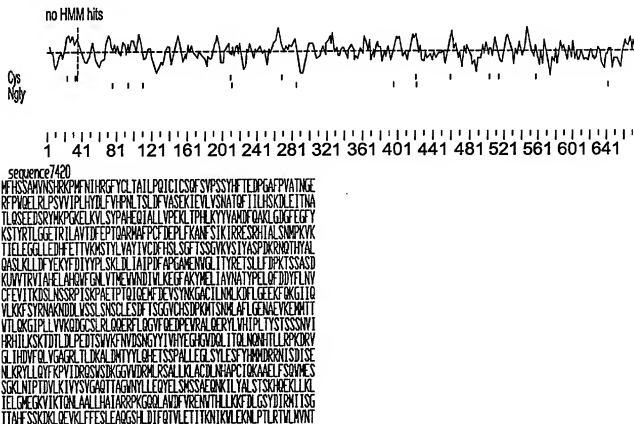


FIG. 3.

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Prosite Pattern Matches for sequence7420

>PS00001/PDCC00001/ASN_GLYCOSYLATION N-glycosylation site.

Query:	85	NLTS	88
Query:	103	NATQ	106
Query:	119	NATL	122
Query:	219	NFSI	222
Query:	294	NQTH	297

FIG. 4A.

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Query: 405 NATY 408
 Query: 431 NSSR 434
 Query: 650 NHTL 653
 Query: 714 NISD 717
 Query: 879 NWTB 882

>PS00004/PDOC00004/CAMP_PHOSPHO_SITE cAMP - and cGMP-dependent protein kinase phosphorylation site.

Query: 225 RRES 228
 Query: 483 KKFS 486

>PS00005/PDOC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 10 SHR 12
 Query: 94 SEK 96
 Query: 183 TYR 185
 Query: 221 SIK 223
 Query: 256 TVK 258
 Query: 303 SLK 305
 Query: 343 TYR 345
 Query: 359 SDK 361
 Query: 432 SSR 434
 Query: 486 SYR 488
 Query: 558 SLR 560
 Query: 740 SDK 742
 Query: 781 SGK 783
 Query: 830 TSK 832
 Query: 906 SSK 908
 Query: 951 TLR 853

>PS00006/PDOC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 57 TNGE 60
 Query: 87 TSLD 90
 Query: 124 SEED 127
 Query: 197 TDFE 200
 Query: 321 SKLD 324
 Query: 343 TYRE 346
 Query: 357 SASD 360
 Query: 407 TYPE 410
 Query: 502 SCLE 505
 Query: 607 SKTD 610
 Query: 701 SYLE 704
 Query: 738 SWSO 741
 Query: 744 SVVD 747
 Query: 817 SSAE 820

FIG. 4B.

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Query: 906 SSKD 909
 Query: 926 SHLD 929
 Query: 933 TVLE 936

>PS00007/PDOC00007/TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 312 KYFDIYY 318
 Query: 622 KFNVDNGY 630
 Query: 679 KALDMTY 686
 Query: 885 KKFILGSY 892

>PS00008/PDOC00008/MYRISTYL N-myristoylation site.

Query: 281 GVKVSI 286
 Query: 334 GAMENW 339
 Query: 378 GNLVTM 383
 Query: 512 GVCHSD 517
 Query: 798 GAQTTA 803
 Query: 868 GQQLAW 873

>PS00142/PDOC00129/ZINC_PROTEASE Neutral zinc metalloproteinases, zinc-binding region signature.

Query: 367 VIAHIAHGW 376

FIG. 4C.

10036072.123103

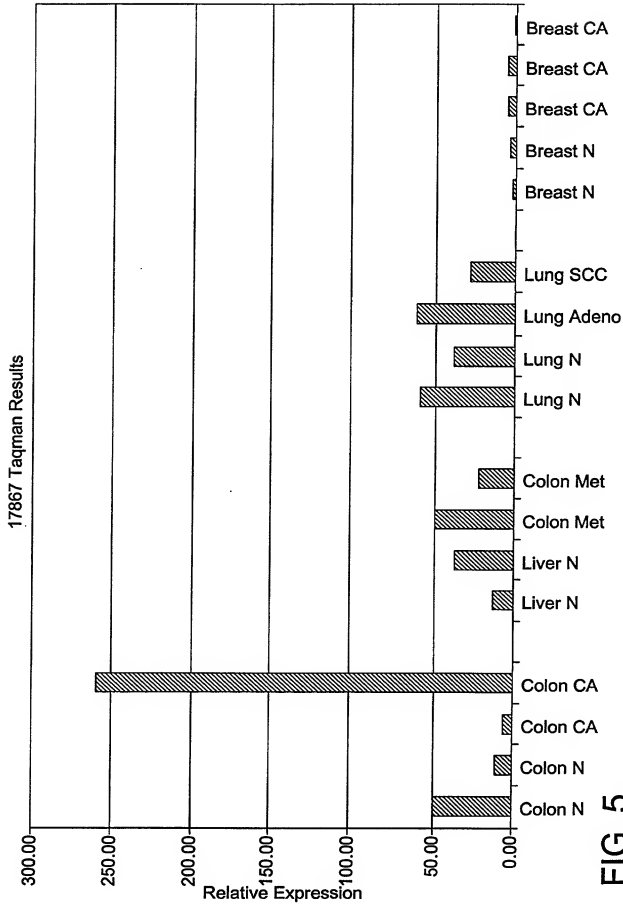


FIG. 5.

